EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	0	("(GeorgeNCox).inv.").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/26 21:29
L2	40	(george N Cox).inv.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/26 21:29
S1	117	(interleukin-11).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/26 21:29
S2	10	(interleukin-11 PEG).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/25 12:39
S3	1	("6608183").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/25 13:00
S4	1	("5206344").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/25 13:01
S5	1	("5166322").PN.	US-PGPUB; USPAT; EPO; JPO	OR	OFF	2006/09/25 13:01
S6	4	(interleukin-11 cysteine added variant).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/25 14:21
S7	5	(interleukin-11 cysteine variant).clm.	US-PGPUB; USPAT; EPO; JPO; DERWENT	AND	OFF	2006/09/25 14:21

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        (FILE 'HOME' ENTERED AT 21:49:49 ON 26 SEP 2006)

        FILE 'MEDLINE, BIOSIS, EMBASE, CAPLUS' ENTERED AT 21:50:02 ON 26 SEP 2006
L1          86 S COX G N/AU
L2          43 DUP REM L1 (43 DUPLICATES REMOVED)
L3        4345 S IL-11
L4           3 S (CYSTEINE ADDED VARIANT)
L5           0 S L3 AND L4
L6        8664 S PEGYLATED
L7          16 S L3 AND L6
L8           7 DUP REM L7 (9 DUPLICATES REMOVED)
L9           0 S (IL-11 VARIANT)
L10          0 S (IL-11 PEG)
L11         16 S (IL-11 AND PEG)
L12          8 DUP REM L11 (8 DUPLICATES REMOVED)
L13          0 S (PEG-IL11)
L14          0 S (IL-11 AND PEG AND VARIANT)
L15          3 S L1 AND L6

=> logoff
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SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rag.

This page gives you Search Results detail for the Application 10773939 and Search Result us-10-773-939-17.rag.

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                        GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:        September 21, 2006, 09:55:14 ; Search time 198 Seconds
                                             (without alignments)
                                             459.526 Million cell updates/sec

Title:         US-10-773-939-17
Perfect score: 1025
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Scoring table: BLOSUM62
               Gapop 10.0 , Gapext 0.5

Searched:      2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters:      2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                          SUMMARIES
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6	1025	100.0	199	7	ADC78851		Adc78851 Human PRO
7	1025	100.0	199	7	ADF70854		Adf70854 Human int
8	1025	100.0	199	8	ADL16724		Adl16724 Human int
9	1025	100.0	199	8	ADQ19047		Adq19047 Human sof
10	1025	100.0	199	9	ADX16342		Adx16342 Full leng
11	1025	100.0	199	9	ADY93813		Ady93813 Human int
12	1022	99.7	199	2	AAR24436		Aar24436 Sequence
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42	907	88.5	786	9	AEA61935		Aea61935 Interleuk
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ALIGNMENTS

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ID   AAR12314 standard; protein; 199 AA.
XX
AC   AAR12314;
XX
DT   25-MAR-2003 (revised)

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rai.

This page gives you Search Results detail for the Application 10773939 and Search Result us-10-773-939-17.rai.

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                        GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:          September 21, 2006, 10:04:03 ; Search time 49 Seconds
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                                              355.482 Million cell updates/sec

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Perfect score:   1025
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Scoring table:   BLOSUM62
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Total number of hits satisfying chosen parameters:       650591

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Post-processing: Minimum Match 0%
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       Pred. No. is the number of results predicted by chance to have a
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   15      963    94.0    199   1   US-07-949-516A-2        Sequence 2, Appli
   16      963    94.0    199   1   US-08-814-459-2         Sequence 2, Appli
   17      963    94.0    199   2   US-09-122-525-2         Sequence 2, Appli
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   19      963    94.0    199   7   5215895-4               Patent No. 5215895
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   36      106    10.3    827   3   US-10-171-384-3         Sequence 3, Appli
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ALIGNMENTS

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; Sequence 4, Application US/08017522A
; Patent No. 5371193
;   GENERAL INFORMATION:
;   APPLICANT: BENNETT, FRANCES K
;   APPLICANT: PAUL, STEPHAN R
;   APPLICANT: YANG, YU-CHUNG
;   TITLE OF INVENTION: A MAMMALIAN CYTOKINE, IL-11
;   NUMBER OF SEQUENCES: 4

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rapbm.

This page gives you Search Results detail for the Application 10773939 and Search Result us-10-7;
17.rapbm.

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OM protein - protein search, using sw model

Run on:          September 21, 2006, 10:04:41 ; Search time 172 Seconds
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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.


                             SUMMARIES
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22	898	87.6	199	3	US-09-791-497-6	Sequence 6, Appli
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26	107	10.4	1042	4	US-10-282-122A-61918	Sequence 61918, A
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ALIGNMENTS

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; Sequence 5, Application US/09791497
; Publication No. US20030008343A1
; GENERAL INFORMATION:
;   APPLICANT: Timans, Jacqueline C.
;   APPLICANT: Kastelein, Robert A.
;   APPLICANT: Bazan, J. Fernando
;   APPLICANT: Pflanz, Stefan
;   TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
;   FILE REFERENCE: DX01040K2
;   CURRENT APPLICATION NUMBER: US/09/791,497

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rapbn.

This page gives you Search Results detail for the Application 10773939 and Search Result us-10-773-939-17.rapbn.

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OM protein - protein search, using sw model

Run on:         September 21, 2006, 10:05:36 ; Search time 34 Seconds
                                        (without alignments)
                                        416.508 Million cell updates/sec

Title:          US-10-773-939-17
Perfect score:  1025
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Total number of hits satisfying chosen parameters:       260401

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                             SUMMARIES
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Result          Query
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6	102	10.0	321	7	US-11-056-355B-9780	Sequence 9780, Ap
7	102	10.0	376	6	US-10-953-349-35327	Sequence 35327, A
8	102	10.0	376	7	US-11-056-355B-9779	Sequence 9779, Ap
9	100.5	9.8	1089	6	US-10-196-749-266	Sequence 266, App
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16	94.5	9.2	1036	7	US-11-121-133-256	Sequence 256, App
17	94	9.2	252	7	US-11-036-257-75	Sequence 75, Appl
18	92.5	9.0	206	7	US-11-056-355B-1369	Sequence 1369, Ap
19	92.5	9.0	1154	7	US-11-301-457-23	Sequence 23, Appl
20	92	9.0	933	6	US-10-526-905-15	Sequence 15, Appl
21	92	9.0	933	7	US-11-283-329-106	Sequence 106, App
22	92	9.0	1360	7	US-11-330-403-4001	Sequence 4001, Ap
23	92	9.0	3575	7	US-11-330-403-5161	Sequence 5161, Ap
24	91	8.9	614	6	US-10-449-902-51430	Sequence 51430, A
25	90.5	8.8	819	6	US-10-449-902-56721	Sequence 56721, A
26	89	8.7	265	7	US-11-056-355B-2446	Sequence 2446, Ap
27	88.5	8.6	193	7	US-11-056-355B-59910	Sequence 59910, A
28	88.5	8.6	198	7	US-11-056-355B-59909	Sequence 59909, A
29	88.5	8.6	222	7	US-11-056-355B-59908	Sequence 59908, A
30	88.5	8.6	2082	7	US-11-330-403-9531	Sequence 9531, Ap
31	87.5	8.5	154	6	US-10-953-349-38409	Sequence 38409, A
32	87.5	8.5	398	7	US-11-330-403-18597	Sequence 18597, A
33	87.5	8.5	871	7	US-11-330-403-2899	Sequence 2899, Ap
34	87	8.5	225	7	US-11-056-355B-62339	Sequence 62339, A
35	87	8.5	743	7	US-11-121-133-164	Sequence 164, App
36	87	8.5	743	7	US-11-121-133-254	Sequence 254, App
37	87	8.5	1015	6	US-10-505-928-359	Sequence 359, App
38	87	8.5	3792	7	US-11-330-623-10	Sequence 10, Appl
39	86.5	8.4	485	7	US-11-056-355B-66410	Sequence 66410, A
40	86.5	8.4	519	6	US-10-526-940-9	Sequence 9, Appli
41	86	8.4	249	7	US-11-056-355B-15700	Sequence 15700, A
42	86	8.4	404	7	US-11-056-355B-15699	Sequence 15699, A
43	86	8.4	409	7	US-11-056-355B-15698	Sequence 15698, A
44	86	8.4	481	6	US-10-449-902-29923	Sequence 29923, A
45	86	8.4	481	6	US-10-449-902-54571	Sequence 54571, A

ALIGNMENTS

RESULT 1
US-11-300-928-18
; Sequence 18, Application US/11300928
; Publication No. US20060166277A1
; GENERAL INFORMATION:
; APPLICANT: Karumanchi, S. Ananth
; APPLICANT: Sukhatme, Vikas P.
; TITLE OF INVENTION: Nucleic Acids and Polypeptides Useful For Diagnosing and Treati
; TITLE OF INVENTION: Complications of Pregnancy

SCORE Search Results Details for Application 10773939 and Search Result us-10-773-939-17.rup.

This page gives you Search Results detail for the Application 10773939 and Search Result us-10-773-939-17.rup.

start

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                    GenCore version 5.1.9
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OM protein - protein search, using sw model

Run on:      ·    September 21, 2006, 09:55:14 ; Search time 298 Seconds ·
                                               (without alignments)
                                              617.712 Million cell updates/sec

Title:           US-10-773-939-17
Perfect score:   1025
Sequence:        1 MNCVCRLVLVVLSLWPDTAV..........GLHLTLDWAVRGLLLLKTRL 199

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters:       2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_7.2:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                             SUMMARIES
                    %
Result           Query
  No.    Score  Match Length DB  ID                      Description
-------------------------------------------------------------------------------
       1  1025  100.0    199  1  IL11_HUMAN              P20809 homo sapien
       2  1014   98.9    199  2  Q96EB4_HUMAN            Q96eb4 homo sapien
       3   963   94.0    199  1  IL11_MACFA              P20808 macaca fasc
       4   898   87.6    199  1  IL11_MOUSE              P47873 mus musculu
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5	898	87.6	199	1	IL11_RAT	Q99mf5	rattus norv
6	878	85.7	218	2	Q3V0U3_MOUSE	Q3v0u3	mus musculu
7	183.5	17.9	198	2	Q4H133_CYPCA	Q4h133	cyprinus ca
8	181.5	17.7	204	2	Q5NKG1_ONCMY	Q5nkg1	oncorhynchu
9	159	15.5	201	2	Q494Q9_FUGRU	Q494q9	fugu rubrip
10	159	15.5	219	2	Q494Q5_BRARE	Q494q5	brachydanio
11	149	14.5	1990	2	Q4SN43_TETNG	Q4sn43	tetraodon n
12	147.5	14.4	200	2	Q494Q7_TETNG	Q494q7	tetraodon n
13	120.5	11.8	194	2	Q494Q4_BRARE	Q494q4	brachydanio
14	116.5	11.4	520	2	Q80ZB8_RAT	Q80zb8	rattus norv
15	115	11.2	511	2	Q80ZB9_RAT	Q80zb9	rattus norv
16	115	11.2	837	2	Q63618_RAT	Q63618	rattus norv
17	114.5	11.2	715	2	Q725K1_DESVH	Q725k1	desulfovibr
18	111.5	10.9	320	2	Q2IG12_9DELT	Q2ig12	anaeromyxob
19	110.5	10.8	871	2	Q9ET47_MOUSE	Q9et47	mus musculu
20	110	10.7	375	2	Q4WZQ1_ASPFU	Q4wzq1	aspergillus
21	110	10.7	433	2	Q8T3H9_DROME	Q8t3h9	drosophila
22	110	10.7	1411	2	Q73Y53_MYCPA	Q73y53	mycobacteri
23	110	10.7	5432	2	Q52V52_9ACTO	Q52v52	streptomyce
24	109.5	10.7	763	1	RIN1_MOUSE	Q921q7	mus musculu
25	108.5	10.6	1755	2	Q80WC3_MOUSE	Q80wc3	mus musculu
26	108	10.5	997	2	Q3J6B6_RHOS4	Q3j6b6	rhodobacter
27	108	10.5	1243	2	Q6GQT8_MOUSE	Q6gqt8	mus musculu
28	107.5	10.5	388	2	Q9KZV7_STRCO	Q9kzv7	streptomyce
29	107	10.4	275	2	Q5Z4H2_ORYSA	Q5z4h2	oryza sativ
30	106	10.3	438	2	Q5SIW1_THET8	Q5siw1	thermus the
31	106	10.3	438	2	Q72J90_THET2	Q72j90	thermus the
32	106	10.3	828	1	IASPP_HUMAN	Q8wuf5	homo sapien
33	106	10.3	828	2	Q2PNZ9_HUMAN	Q2pnz9	homo sapien
34	106	10.3	969	2	Q4VBD6_MOUSE	Q4vbd6	mus musculu
35	105.5	10.3	571	2	Q96AX3_HUMAN	Q96ax3	homo sapien
36	105.5	10.3	871	2	Q96S23_HUMAN	Q96s23	homo sapien
37	105	10.2	1003	2	Q3TY92_MOUSE	Q3ty92	mus musculu
38	104.5	10.2	341	2	Q3W467_9ACTO	Q3w467	frankia sp.
39	104	10.1	783	2	Q9VPX6_DROME	Q9vpx6	drosophila
40	103.5	10.1	832	2	Q9VNC4_DROME	Q9vnc4	drosophila
41	103.5	10.1	1322	2	Q5K7E6_CRYNE	Q5k7e6	cryptococcu
42	103.5	10.1	7510	2	Q52V50_9ACTO	Q52v50	streptomyce
43	102.5	10.0	303	2	Q4K7J6_PSEF5	Q4k7j6	pseudomonas
44	102.5	10.0	4613	2	Q9ZGI5_9ACTO	Q9zgi5	streptomyce
45	101.5	9.9	208	2	Q6UAM0_TETNG	Q6uam0	tetraodon n

ALIGNMENTS

RESULT 1
IL11_HUMAN
ID   IL11_HUMAN   STANDARD;   PRT;   199 AA.
AC   P20809;
DT   01-FEB-1991, integrated into UniProtKB/Swiss-Prot.
DT   01-FEB-1991, sequence version 1.
DT   07-FEB-2006, entry version 55.
DE   Interleukin-11 precursor (IL-11) (Adipogenesis inhibitory factor)
DE   (AGIF) (Oprelvekin).
GN   Name=IL11;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;